

Rec'd PCT/PTO 13 APR 2005

10/530393

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/530,393

Source: PG/10

Date Processed by STIC: 4/13/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 04/13/2005

PATENT APPLICATION: US/10/530,393

TIME: 09:42:26

Input Set : D:\8449304999.txt

Output Set: N:\CRF4\04132005\J530393.raw

3 <110> APPLICANT: LeClair, Ken
 4 Srivastava, Pramod K.
 6 <120> TITLE OF INVENTION: Heat Shock Protein Binding Fragments of CD91, and Uses
 Thereof
 8 <130> FILE REFERENCE: 8449-304-999
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/530,393
 C--> 10 <141> CURRENT FILING DATE: 2005-04-04
 10 <150> PRIOR APPLICATION NUMBER: PCT/US03/32167
 11 <151> PRIOR FILING DATE: 2003-10-07
 13 <150> PRIOR APPLICATION NUMBER: 60/416,821
 14 <151> PRIOR FILING DATE: 2002-10-07
 16 <160> NUMBER OF SEQ ID NOS: 17
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2553
 22 <212> TYPE: DNA
 23 <213> ORGANISM: H. sapiens
 25 <400> SEQUENCE: 1
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 28 atcgacgccc ctaagacttg cagccccaag cagtttgctt gcagagatca aataacctgt 120
 30 atctcaaagg gctggcggtg cgacggtgag agggactgcc cagacggatc tgacgaggcc 180
 32 cctgagattt gtccacagag taaggccagc cgatgccagc caaacgagca taactgcctg 240
 34 ggtactgagc tgtgtgttcc catgtcccgc ctctgcaatg ggggtccagga ctgcatggac 300
 36 ggctcagatg aggggcccac ctgccgagag ctccaaggca actgctctcg cctgggctgc 360
 38 cagcaccatt gtgtccccac actcgatggg cccacctgct actgcaacag cagctttcag 420
 40 cttcaggcag atggcaagac ctgcaaagat tttgatgagt gctcagtgtg cggcacctgc 480
 42 agccagctat gcaccaacac agacggctcc ttcatatgtg gctgtgttga aggatacctc 540
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 46 ctgttgatag ccaactccca gaacatcttg gccacgtacc tgagtggggc ccaggtgtct 660
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 52 atgcctggcc taaagggtt cgtggatgag cacaccatca acatctccct cagtctgcac 840
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78 aagccggagc atgagctgtt cctcgtgtat ggcaagggcc ggccaggcat catccggggc 1620
80 atggatatgg gggccaaggt cccggatgag cacatgatcc ccattgaaaa cctcatgaac 1680
82 ccccgagccc tggacttcca cgctgagacc ggcttcatct actttgccga caccaccagc 1740
84 tacctcattg gccgccagaa gattgatggc actgagcggg agaccatcct gaaggacggc 1800
86 atccacaatg tggagggtgt ggccgtggac tggatgggag acaatctgta ctggacggac 1860
88 gatgggcccc aaaagacaat cagcgtggcc aggctggaga aagctgctca gaccgcgaag 1920
90 actttaatcg agggcaaaat gacacacccc agggctattg tggatggatcc actcaatggg 1980
92 tggatgtact ggacagactg ggaggaggac cccaaggaca gtcggcgtgg gcggctggag 2040
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96 cccaatgggc taagcctgga catcccggtt gggcgctct actgggtgga tgccttctac 2160
98 gaccgcacg agacgatact gctcaatggc acagaccgga agattgtgta tgaaggctct 2220
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113 <210> SEQ ID NO: 2

114 <211> LENGTH: 851

115 <212> TYPE: PRT

116 <213> ORGANISM: H. sapiens

118 <400> SEQUENCE: 2

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124 Ala Ala Ala Ala Ile Asp Ala Pro Lys Thr Cys Ser Pro Lys Gln Phe
125 20 25 30
128 Ala Cys Arg Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp
129 35 40 45
132 Gly Glu Arg Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys
133 50 55 60
136 Pro Gln Ser Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu
137 65 70 75 80
140 Gly Thr Glu Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln
141 85 90 95
144 Asp Cys Met Asp Gly Ser Asp Glu Gly Pro His Cys Arg Glu Leu Gln
145 100 105 110
148 Gly Asn Cys Ser Arg Leu Gly Cys Gln His His Cys Val Pro Thr Leu
149 115 120 125
152 Asp Gly Pro Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp
153 130 135 140
156 Gly Lys Thr Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys
157 145 150 155 160
160 Ser Gln Leu Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val
161 165 170 175
164 Glu Gly Tyr Leu Leu Gln Pro Asp Asn Arg Ser Cys Lys Ala Lys Asn
165 180 185 190
168 Glu Pro Val Asp Arg Pro Pro Val Leu Leu Ile Ala Asn Ser Gln Asn
169 195 200 205
172 Ile Leu Ala Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro

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176 Thr Ser Thr Arg Gln Thr Thr Ala Met Asp Phe Ser Tyr Ala Asn Glu
177 225      230      235      240
180 Thr Val Cys Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu
181      245      250      255
184 Lys Cys Ala Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr
185      260      265      270
188 Ile Asn Ile Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp
189      275      280      285
192 Trp Leu Thr Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile
193      290      295      300
196 Phe Val Cys Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu
197 305      310      315      320
200 Glu Leu Tyr Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys
201      325      330      335
204 Val Phe Phe Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp
205      340      345      350
208 Met Asp Gly Gln Asn Arg Thr Lys Leu Val Asp Ser Lys Ile Val Phe
209      355      360      365
212 Pro His Gly Ile Thr Leu Asp Leu Val Ser Arg Leu Val Tyr Trp Ala
213      370      375      380
216 Asp Ala Tyr Leu Asp Tyr Ile Glu Val Val Asp Tyr Glu Gly Lys Gly
217 385      390      395      400
220 Arg Gln Thr Ile Ile Gln Gly Ile Leu Ile Glu His Leu Tyr Gly Leu
221      405      410      415
224 Thr Val Phe Glu Asn Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Ala Asn
225      420      425      430
228 Ala Gln Gln Lys Thr Ser Val Ile Arg Val Asn Arg Phe Asn Ser Thr
229      435      440      445
232 Glu Tyr Gln Val Val Thr Arg Val Asp Lys Gly Gly Ala Leu His Ile
233      450      455      460
236 Tyr His Gln Arg Arg Gln Pro Arg Val Arg Ser His Ala Cys Glu Asn
237 465      470      475      480
240 Asp Gln Tyr Gly Lys Pro Gly Gly Cys Ser Asp Ile Cys Leu Leu Ala
241      485      490      495
244 Asn Ser His Lys Ala Arg Thr Cys Arg Cys Arg Ser Gly Phe Ser Leu
245      500      505      510
248 Gly Ser Asp Gly Lys Ser Cys Lys Lys Pro Glu His Glu Leu Phe Leu
249      515      520      525
252 Val Tyr Gly Lys Gly Arg Pro Gly Ile Ile Arg Gly Met Asp Met Gly
253      530      535      540
256 Ala Lys Val Pro Asp Glu His Met Ile Pro Ile Glu Asn Leu Met Asn
257 545      550      555      560
260 Pro Arg Ala Leu Asp Phe His Ala Glu Thr Gly Phe Ile Tyr Phe Ala
261      565      570      575
264 Asp Thr Thr Ser Tyr Leu Ile Gly Arg Gln Lys Ile Asp Gly Thr Glu
265      580      585      590
268 Arg Glu Thr Ile Leu Lys Asp Gly Ile His Asn Val Glu Gly Val Ala
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272 Val Asp Trp Met Gly Asp Asn Leu Tyr Trp Thr Asp Asp Gly Pro Lys
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276 Lys Thr Ile Ser Val Ala Arg Leu Glu Lys Ala Ala Gln Thr Arg Lys
277 625                      630                      635                      640
280 Thr Leu Ile Glu Gly Lys Met Thr His Pro Arg Ala Ile Met Val Asp
281      645                      650                      655
284 Pro Leu Asn Gly Trp Met Tyr Trp Thr Asp Trp Glu Glu Asp Pro Lys
285      660                      665                      670
288 Asp Ser Arg Arg Gly Arg Leu Glu Arg Ala Trp Met Asp Gly Ser His
289      675                      680                      685
292 Arg Asp Ile Phe Val Thr Ser Lys Thr Val Leu Trp Pro Asn Gly Leu
293 690                      695                      700
296 Ser Leu Asp Ile Pro Ala Gly Arg Leu Tyr Trp Val Asp Ala Phe Tyr
297 705                      710                      715                      720
300 Asp Arg Ile Glu Thr Ile Leu Leu Asn Gly Thr Asp Arg Lys Ile Val
301      725                      730                      735
304 Tyr Glu Gly Pro Glu Leu Asn His Ala Phe Gly Leu Cys His His Gly
305      740                      745                      750
308 Asn Tyr Leu Phe Trp Thr Glu Tyr Arg Ser Gly Ser Val Tyr Arg Leu
309      755                      760                      765
312 Glu Arg Gly Val Gly Gly Ala Pro Pro Thr Val Thr Leu Leu Arg Ser
313 770                      775                      780
316 Glu Arg Pro Pro Ile Phe Glu Ile Arg Met Tyr Asp Ala Gln Gln Gln
317 785                      790                      795                      800
320 Gln Val Gly Thr Asn Lys Cys Arg Val Asn Asn Gly Gly Cys Ser Ser
321      805                      810                      815
324 Leu Cys Leu Ala Thr Pro Gly Ser Arg Gln Cys Ala Cys Ala Glu Asp
325      820                      825                      830
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329      835                      840                      845
332 Val Pro Pro
333      850
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 896
338 <212> TYPE: PRT
339 <213> ORGANISM: H. sapiens
341 <400> SEQUENCE: 3
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347 Ala Ala Ala Ala Ile Asp Ala Pro Lys Thr Cys Ser Pro Lys Gln Phe
348      20      25      30
351 Ala Cys Arg Asp Gln Ile Thr Cys Ile Ser Lys Gly Trp Arg Cys Asp
352      35      40      45
355 Gly Glu Arg Asp Cys Pro Asp Gly Ser Asp Glu Ala Pro Glu Ile Cys
356      50      55      60
359 Pro Gln Ser Lys Ala Gln Arg Cys Gln Pro Asn Glu His Asn Cys Leu
360 65      70      75      80
363 Gly Thr Glu Leu Cys Val Pro Met Ser Arg Leu Cys Asn Gly Val Gln
364      85      90      95

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367 Asp Cys Met Asp Gly Ser Asp Glu Gly Pro His Cys Arg Glu Leu Gln
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371 Gly Asn Cys Ser Arg Leu Gly Cys Gln His His Cys Val Pro Thr Leu
372      115      120      125
375 Asp Gly Pro Thr Cys Tyr Cys Asn Ser Ser Phe Gln Leu Gln Ala Asp
376      130      135      140
379 Gly Lys Thr Cys Lys Asp Phe Asp Glu Cys Ser Val Tyr Gly Thr Cys
380 145      150      155      160
383 Ser Gln Leu Cys Thr Asn Thr Asp Gly Ser Phe Ile Cys Gly Cys Val
384      165      170      175
387 Glu Gly Tyr Leu Leu Gln Pro Asp Asn Arg Ser Cys Lys Ala Lys Asn
388      180      185      190
391 Glu Pro Val Asp Arg Pro Pro Val Leu Leu Ile Ala Asn Ser Gln Asn
392      195      200      205
395 Ile Leu Ala Thr Tyr Leu Ser Gly Ala Gln Val Ser Thr Ile Thr Pro
396      210      215      220
399 Thr Ser Thr Arg Gln Thr Thr Ala Met Asp Phe Ser Tyr Ala Asn Glu
400 225      230      235      240
403 Thr Val Cys Trp Val His Val Gly Asp Ser Ala Ala Gln Thr Gln Leu
404      245      250      255
407 Lys Cys Ala Arg Met Pro Gly Leu Lys Gly Phe Val Asp Glu His Thr
408      260      265      270
411 Ile Asn Ile Ser Leu Ser Leu His His Val Glu Gln Met Ala Ile Asp
412      275      280      285
415 Trp Leu Thr Gly Asn Phe Tyr Phe Val Asp Asp Ile Asp Asp Arg Ile
416      290      295      300
419 Phe Val Cys Asn Arg Asn Gly Asp Thr Cys Val Thr Leu Leu Asp Leu
420 305      310      315      320
423 Glu Leu Tyr Asn Pro Lys Gly Ile Ala Leu Asp Pro Ala Met Gly Lys
424      325      330      335
427 Val Phe Phe Thr Asp Tyr Gly Gln Ile Pro Lys Val Glu Arg Cys Asp
428      340      345      350
431 Met Asp Gly Gln Asn Arg Thr Lys Leu Val Asp Ser Lys Ile Val Phe
432      355      360      365
435 Pro His Gly Ile Thr Leu Asp Leu Val Ser Arg Leu Val Tyr Trp Ala
436      370      375      380
439 Asp Ala Tyr Leu Asp Tyr Ile Glu Val Val Asp Tyr Glu Gly Lys Gly
440 385      390      395      400
443 Arg Gln Thr Ile Ile Gln Gly Ile Leu Ile Glu His Leu Tyr Gly Leu
444      405      410      415
447 Thr Val Phe Glu Asn Tyr Leu Tyr Ala Thr Asn Ser Asp Asn Ala Asn
448      420      425      430
451 Ala Gln Gln Lys Thr Ser Val Ile Arg Val Asn Arg Phe Asn Ser Thr
452      435      440      445
455 Glu Tyr Gln Val Val Thr Arg Val Asp Lys Gly Gly Ala Leu His Ile
456      450      455      460
459 Tyr His Gln Arg Arg Gln Pro Arg Val Arg Ser His Ala Cys Glu Asn
460 465      470      475      480
463 Asp Gln Tyr Gly Lys Pro Gly Gly Cys Ser Asp Ile Cys Leu Leu Ala

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date